Foot-and-Mouth Disease

October-December 2020
Quarterly report

FAST Reports
Foot-and-mouth And Similar Transboundary animal diseases

European Commission for the Control of Foot-and-Mouth Disease
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<th>Abbreviation</th>
<th>Description</th>
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<tr>
<td>BVI</td>
<td>Botswana Vaccine Institute</td>
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<td>EIDRA</td>
<td>Emerging Infectious Disease Research Association</td>
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<td>EuFMD</td>
<td>European Commission for the Control of Foot-and-Mouth Disease</td>
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<td>FAST reports</td>
<td>Foot-and-mouth and similar transboundary animal diseases reports</td>
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<td>FGBI “ARRIAH”</td>
<td>Federal Governmental Budgetary Institution “Federal Centre for Animal Health”</td>
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<td>FMD</td>
<td>Foot-and-mouth disease</td>
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<td>FMDV</td>
<td>Foot-and-mouth disease Virus</td>
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<td>FMDV GD</td>
<td>Foot-and-mouth disease Virus Genome detected</td>
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<tr>
<td>FMDV NGD</td>
<td>Foot-and-mouth disease Virus Genome not detected</td>
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<td>GF-TAD</td>
<td>Global Framework for the Progressive Control of Transboundary Animal Diseases</td>
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<td>LVRI</td>
<td>The National Reference Laboratory for FMD, The Lanzhou Veterinary Research Institute, Chinese Academy of Agricultural Sciences</td>
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<td>MEVAC</td>
<td>International Facility for Veterinary Vaccines Production (Egypt)</td>
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<tr>
<td>NT</td>
<td>Not tested</td>
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<tr>
<td>NVD</td>
<td>No virus detected</td>
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<td>OIE</td>
<td>World Organisation for Animal Health</td>
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<td>PIADC</td>
<td>Plum Island Animal Disease Center</td>
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<td>rRT-PCR</td>
<td>Real-time reverse transcription polymerase chain reaction</td>
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<td>SAARC</td>
<td>South Asian Association for Regional Cooperation</td>
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<td>SADC</td>
<td>Southern Africa in collaboration with the Southern African Development Community</td>
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<td>SAT</td>
<td>Southern African Territories</td>
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<td>South-East Asia and China FMD campaign</td>
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<td>SSARRL</td>
<td>Sub-Saharan Africa Regional Reference Laboratory</td>
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<td>SVD</td>
<td>Swine vesicular disease</td>
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<td>VETBIS</td>
<td>Veterinary Information System of Turkey</td>
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<td>VI</td>
<td>Virus Isolation</td>
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<td>WAHIS</td>
<td>World Animal Health Information System (of the OIE)</td>
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<td>WRLFMD</td>
<td>World Reference Laboratory for Foot-and-Mouth Disease</td>
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1. Highlights and headlines

Welcome to the first issue of the FMD Quarterly Report for 2021 and I take the opportunity to pass on my best wishes for the New Year. Despite the limitations placed on all of us by the COVID-19 pandemic, I was very pleased to be able to catch-up with many FMD colleagues via a series of meetings in “virtual” format organised at the end of 2020 - including the EU-RL Workshop (organised by ANSES and Sciensano), the Annual meeting of the OIE/FAO FMD Laboratory Network (www.foot-and-mouth.org), the 25th SEACFMD sub-commission meeting and the Open Session of EuFMD (https://www.eufmd.info/os20faster).

This report describes the latest intelligence and results from samples collected from FMD endemic countries. In recent years, particular attention has focused on FMD viruses that circulate in Pool 2 (South Asia) and the frequency by which these viruses can seed new outbreaks elsewhere in Asia. Examples of viruses that have spread from Pool 2 include O/ME-SA/Ind-2001 (d and e sub-lineages) and A/ASIA/G-VII. Earlier in 2020, a new serotype O lineage was described for samples collected in Sri Lanka (see Jan-Mar 2020 report); new data provided from ICAR-DFMD India during the OIE/FAO FMD Laboratory Network meeting provides further evidence that this lineage (tentatively named O/ME-SA-SA-2018) is more widely distributed in South Asian countries. Data in this report also describes new genetic clade within the O/ME-SA/PanAsia sub-lineage which has been detected in Iran and presents the phylogenetic tree for the new cases due to the O/ME-SA/PanAsia sub-lineage detected in Turkey. Elsewhere, sub-clinical cases (due to SAT 1) have been reported in South Africa.

The WRLFMD has been recently working with EuFMD to develop an open-access interactive FMD dashboard to allow users to interrogate, retrieve and display FMD information (including FMDV genomic data). The scope and functionality of the improved tools implemented during this project will be influenced by your requirements and therefore we are seeking feedback to help us to understand how we should prioritise the design of this system. For those you that are interested, please complete the survey in the link: https://forms.office.com/Pages/ResponsePage.aspx?id=Eh70v1zu20izMQzOHucOut-jsc2qwZOo151ynO2MwhUN01SUFVROTc3TTTRYRklEMTU3WU1FTUsyQy4u

Don King, Pirbright January 2021

Figure 1: Recent headline events (reported October-December 2020) with endemic pools highlighted in orange. Source: WRLFMD. Map conforms to the United Nations World Map, June 2020.
2. General overview

Endemic Pools represent independently circulating and evolving foot-and-mouth disease virus (FMDV) genotypes; within the pools, cycles of emergence and spread occur that usually affect multiple countries in the region. In the absence of specific reports, it should be assumed that the serotypes indicated below are continuously circulating in parts of the pool area and would be detected if sufficient surveillance was in place.

<table>
<thead>
<tr>
<th>POOL</th>
<th>REGION/COUNTRIES</th>
<th>SEROTYPES PRESENT</th>
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<tbody>
<tr>
<td>1</td>
<td>SOUTHEAST ASIA/CENTRAL ASIA/EAST ASIA&lt;br&gt;Cambodia, China, China (Hong Kong SAR), Taiwan Province of China, Democratic People's Republic of Korea, Republic of Korea, Lao People's Democratic Republic, Malaysia, Mongolia, Myanmar, Russian Federation, Thailand, Viet Nam</td>
<td>A, Asia 1 and O</td>
</tr>
<tr>
<td>2</td>
<td>SOUTH ASIA&lt;br&gt;Bangladesh, Bhutan, India, Mauritius, Nepal, Sri Lanka</td>
<td>A, Asia 1 and O</td>
</tr>
<tr>
<td>3</td>
<td>WEST EURASIA &amp; MIDDLE EAST&lt;br&gt;Afghanistan, Armenia, Azerbaijan, Bahrain, Georgia, Iran (Islamic Republic of), Iraq, Israel, Jordan, Kazakhstan, Kuwait, Kyrgyzstan, Lebanon, Oman, Pakistan, Palestine, Qatar, Saudi Arabia, Syrian Arab Republic, Tajikistan, Turkey, Turkmenistan, United Arab Emirates, Uzbekistan</td>
<td>A, Asia 1 and O (SAT 2)</td>
</tr>
<tr>
<td>4</td>
<td>NORTH AFRICA&lt;br&gt;Algeria, Egypt, Libya, Morocco, Tunisia</td>
<td>A, O and SAT 2</td>
</tr>
<tr>
<td>5</td>
<td>WEST/CENTRAL AFRICA&lt;br&gt;Benin, Burkina Faso, Cabo Verde, Cameroon, Central African Republic, Chad, Congo, Côte d'Ivoire, Democratic Republic of the Congo, Equatorial Guinea, Gabon, Gambia, Ghana, Guinea, Guinea-Bissau, Liberia, Mali, Mauritania, Niger, Nigeria, Sao Tome and Principe, Senegal, Sierra Leone, Togo</td>
<td>O, A, SAT 1 and SAT 2</td>
</tr>
<tr>
<td>6</td>
<td>SOUTHERN AFRICA&lt;br&gt;Angola, Botswana, Malawi, Mozambique, Namibia, South Africa, Zambia, Zimbabwe</td>
<td>SAT 1, SAT 2 and SAT 3 (O, A)†</td>
</tr>
<tr>
<td>7</td>
<td>SOUTH AMERICA&lt;br&gt;Colombia, Venezuela (Bolivarian Republic of)</td>
<td>O and A</td>
</tr>
</tbody>
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† only in Angola and north Zambia as spill-over from pool 4
3. Summary of FMD outbreaks and intelligence

3.1. Global overview of samples received and tested

The location of all samples detailed in this report can be seen on the map below. More detailed maps and sample data, on a country by country basis, can be found in the following sections of this report.

![Figure 2: Samples tested by WRLFMD or reported in this quarter. ● indicates samples analysed; × indicates new outbreaks reported to the OIE, but where results to define the genotype have not been reported; □ indicates reports of FMD from other sources. Shape colours define the serotype detected: ● O; ● A; ● C; ● Asia1, ● SAT1, ● SAT2, ● SAT3, ○ FMD not detected, ● serotype undetermined/not given in the report. Source: WRLFMD. Map conforms to the United Nations World map, June 2020.]

3.2. Pool 1 (Southeast Asia/Central Asia/East Asia)

**The Kingdom of Cambodia**

A batch of nine samples was received to WRLFMD on 22 December 2020. Typing and genotyping is underway and will be reported shortly.

FMD is reported to have affected 707 cattle, causing 34 deaths, in Siem Reap province and 1645 cattle in Pailin province. Veterinary officers have been administering vaccines to cattle in the affected areas.

ProMED post: [20201117.7949239](https://www.promedmail.org/post.php?tid=20201117.7949239)
### The Lao People's Democratic Republic

A batch of five samples was received to WRLFMD on 22 December 2020. Typing and genotyping is underway and will be reported shortly.

### The Kingdom of Thailand

A batch of 16 samples was received to WRLFMD on 22 December 2020. Typing and genotyping is underway and will be reported shortly.

### 3.3. Pool 2 (South Asia)

#### The Republic of India

The ICAR-Directorate of Foot-and-Mouth Disease, recently published a study of **FMD type O** in which 286 VP1 sequences were reported (Dahiya *et al.*, 2020). Genotyping showed that all sequences belonged to the ME-SA topotype; two belonged to the PanAsia lineage, 271 to the Ind-2001 lineage (60 were ‘d’ sublineage and 211 were ‘e’ sublineage). Additionally, 13 sequences belonged to a new lineage which we have named O/ME-SA/SA-2018 (SA for South Asia). Exchange of sequence data at the OIE/FAO FMD Laboratory Network meeting (during December) demonstrated that three viruses previously found in Sri Lanka in 2018 and 2019 also belong to this new lineage.


### 3.4. Pool 3 (West Eurasia and Middle East)

#### The Republic of Turkey

Turkey reported the occurrence of 28 FMD outbreaks in cattle (n=21) and small ruminant (7) populations between October and December 2020 (18 in October, 5 in November and 5 in December), among which 21 were confirmed serotype O. This brings the total number of clinical outbreaks in 2020 to 147, with the number of confirmed outbreaks reported to ADNS being 142. (Source: [ADNS](https://www.oie.int/en)). The outbreaks that occurred during the last trimester were distributed in different parts of Anatolia (Ardahan, Bursa, Corum, Denizli, Erzurum, Eskisehir, Isparta, Izmir, Karramanmaras, Kars, Mus, Samsun, Sinop, Tokat, Van, Zondulak
provinces). EuFMD focal points from the Transcaucasus countries were informed about outbreaks in proximity to their borders, as part of the Statement of Intentions between Transcaucasia and neighboring countries (SOI). This triggered targeted control measures, including vaccination, surveillance and awareness raising in the adjoining border regions of the Transcaucasus countries.

FMD is endemic in Anatolia and the circulating sublineages are still believed to be the O PanAsia-2/Qom15 and O PanAsia-2/ANT10 as reported in the previous FAST report. Both are well matched to the vaccines currently in use. Serotypes A and Asia1 were not detected since January 2018 and July 2015, respectively.

On 06 October 2020, six FMD type O VP1 sequences were received from the FMD (Şap) Institute, Ankara. They originated from samples collected from cattle (and one sheep) between December 2019 and September 2020. Genotyping revealed that all belonged to the ME-SA topotype, PanAsia-2 lineage while four sequences belonged to the QOM-15 sublineage (from the provinces of Ardahan, Erzurum, Kars and Mus) and two to the ANT-10 sublineage (from the provinces of Tokat and Van) (see below).

### The Islamic Republic of Iran

During an official meeting with EuFMD on 22 December 2020, the Islamic Republic of Iran reported about 60 FMD outbreaks in large ruminants and 10 outbreaks in small ruminants between October and November 2020. For the first 8 months of 2020, 974 FMD outbreaks were reported in Iran. FMD outbreaks are mostly reported at the end of winter and beginning of spring, due to the combination of more intense livestock movements, increased number of small ruminants (newborns) and more suitable climatic conditions for FMDV environmental survival at these periods. Within the A/ASIA/Iran-05 lineage, the main circulating sublineages identified between January and November 2020 were Sis-12, Sis-13, Far-11 while for O/ME-SA/PanAsia-2, it was Qom-15 and Ant-10. The main Asia 1 lineage was Sindh-08. The O PanAsia-2 Ant-15 sublineage has been predominant between January to November 2020, but the A Iran-05 Far-11 sublineage has been increasingly detected in recent weeks. Implementation of biosecurity measures and vaccination strategies were the main control measures to be applied.

According to the Iran Veterinary Organization (IVO), 6,204,125 large ruminants and 44,599,728 small ruminants were vaccinated against FMD between 1st January and 1st November 2020, using trivalent vaccines (O, A, Asia1) that were either locally produced or imported.

On 25 November 2020, six VP1 sequences of FMD type A were received from Central Veterinary Laboratory of the Iran Veterinary Organisation (CVL-IVO). The samples were collected between May and November 2020 from outbreaks in cattle in the provinces of Ardabil, East Azerbaijan, Qom, Qazvin and West Azerbaijan. Genotyping showed the six sequences belonged to the ASIA topotype, Iran-05 lineage, FAR-11 sublineage (see below).
The Republic of Iraq

Five VP1 sequences were retrieved from GenBank on 23 October 2020. The sequences were derived from nasal swabs collected from bovines in June 2019 and had been submitted by Drs. Abdul-Satar S Sadoon and QT Al-Obaidi of the University of Mosul. Two sequences belonged to FMD type O, one to FMD type Asia 1 and two to FMD type SAT 1. Genotyping showed that the type O viruses belonged to the ME-SA topotype, PanAsia-2 lineage; the Asia 1 viruses belonged to the Sindh-08 lineage; and the SAT 1 viruses belonged to two different topotypes, I (NWZ) and IX (see below). The presence of these virus in Iraq requires confirmation by one of the OIE or FAO reference laboratories.

3.5. Pool 4 (North and Eastern Africa)

The People’s Democratic Republic of Algeria

The last FMD outbreak in Algeria was reported in March 2019 (lineage O EA-3). The vaccination program consists of mass vaccination twice a year for large ruminants (except in 4 southern wilayas) using 6PD50 vaccine (strains O 3039, O Manisa, A 22 Iraq). Between December 2019 and March 2020, 844,734 large ruminants were reportedly vaccinated (representing 60% vaccination coverage). An additional campaign was initiated in October 2020.

The Arab Republic of Egypt

Four FMD outbreaks were detected in 2020, two confirmed as SAT2 serotype and the others confirmed as serotype A. Source: REMESA JPC meeting. The General Organization for Veterinary Services (GOVS) in Egypt conducted sero-surveillance in November 2020 targeting six governorates along the border (Aswan, Matrouh, New Valley, North Sini, South Sini, and Red Sea). The surveillance was supported by EuFMD through the provision of diagnostic kits. The objective of the surveillance was to estimate the serological prevalence to NSP antibodies among the large and small ruminant populations, focusing on the 6-18 months age category. Sera were collected from 1,680 randomly selected animals and tested using a 3ABC NSP ELISA. The results revealed an overall NSP seroprevalence of 10.8% (182/1,680; 95%CI 9.4-12.4%) for small and large ruminants combined. The highest seroprevalence was in Aswan governorate (23.6%) with the lowest being in Matruh governorate.

The State of Libya

Two outbreaks were notified to the OIE on 15th December 2020 (date of start of the outbreaks: 1st November 2020; current status as of 13th January 2021: continuing). Five cases were reported among sheep on two farms located in the Eastern region (Benghazi) with a population of 313 susceptible sheep and 26 goats. Clinical signs included fever, lameness, and abortion in some cases. No genotyping has been reported, but the AFRICA topotype, G-IV lineage has been reported previously.

OIE Immediate notification & Follow-up reports
An investigation team from the National Centre for Animal Health (NCAH), Tripoli visited the areas around the infected premises in Benghazi, Al-Marj, Al-Abyaar, the Gulf of Sirte and Tukra. Sera from 173 cattle, sheep and goats were collected, with 9 sheep and 10 cattle samples from Benghazi and Al-Marj testing positive to NSP antibodies. Structural proteins (SP) ELISA testing to indicate the possible serotype is still pending, noting previous reports identified serotype A as the likely cause. Source: NCAH

Recently, the NCAH adopted a new FMD vaccination strategy, and is planning to receive 400,000 doses to vaccinate the cattle population in Libya (estimated at 100,000 head), providing two doses, two weeks apart. Small ruminants will also be vaccinated using a ring vaccination strategy in response to reported outbreaks. An FMD virtual awareness campaign targeting public and private vets on the topics of FMD diagnosis, sampling, biosecurity, and epidemiology are currently underway, also implemented by the NCAH, in collaboration with EuFMD and the FAO sub-regional office for North Africa.

### Morocco

Morocco renews the OIE endorsed, FMD official control program each year. The last outbreak in Morocco was reported in July 2019. The vaccination strategy uses a bivalent vaccine (strains: O/TUR/2009, A22/IRQ/64. Based on in vitro vaccine matching, the $r_1$ values indicated a good match between the O/TUR/2009 vaccine and strains from the O/Ea-3 lineage circulating in the region. Since 2019, the vaccination program consisted of mass vaccination twice a year for large ruminants (approximately 2.8 million animals) and once yearly risk-based vaccination of small ruminants in border regions in the eastern part of the country (approximately 5 million animals). Morocco conducted post vaccination monitoring studies, with satisfactory results from a small-scale immunogenicity study in 2019 and a population immunity study in 2020.

### Tunisia

No outbreaks were reported in 2020 in Tunisia. The vaccination strategy against FMD consists of annual mass vaccination using 6PD₅₀ trivalent vaccine (strains: O3039, O Manisa, SAT2 Eritrea, A Iraq22) for large ruminants and bivalent (O3039, O Manisa, SAT2 Eritrea) for small ruminants. The reported vaccination coverage in 2020 was 71.2% in large ruminants and 85.7% in small ruminant populations.

### Pool 5 (West/Central Africa)

#### Nigeria

On 25 November 2020, 18 FMDV sequences were received from National Centre for Foreign Animal Disease (NCFAD), Winnipeg, Canada. These were produced in collaboration with the National Veterinary Research Institute (NVRI), Vom, Nigeria. Two sequences were FMD type O, 14 were FMD type A and two were FMD type SAT 2. Genotyping revealed the type O viruses to belong to the WA topotype; the type A viruses all belonged to the AFRICA topotype, G-IV lineage; and the SAT 2 viruses belonged to
Some of the sequences were incomplete VP1’s and are too short to have been included in the trees.

On the 11 December 2020, 25 VP1 sequences were retrieved from GenBank. They had been submitted by the Sciensano Research Institute (Ukkel, Belgium) as part of a joint study with the NVRI. All sequences were derived from samples collected from cattle in the Abuja Federal Capital Territory and the Bauchi, Benue, Kaduna, Oyo and Plateau States between 2013 and 2017. Fourteen were FMD type O, six were FMD type A, three were FMD type SAT 1 and two were FMD type SAT 2. Genotyping showed that two type O viruses belonged to the WA topotype and 12 to the EA-3 topotype; all six type A viruses belonged to the AFRICA topotype, G-IV lineage; the three SAT 1 viruses belonged to topotype X; and the two SAT 2 viruses belonged to topotype VII, Lib-12 lineage (see below).

### 3.7. Pool 6 (Southern Africa)

#### The Republic of Botswana

A single outbreak of FMD type SAT 1 was reported in cattle on 13 September 2020 in Ngamiland (North-West district). VP1 genotyping was performed in the OIE Sub-Saharan Africa Regional Reference laboratory (SSARRL) for FMD at the Botswana Vaccine Institute (BVI) and showed the virus to belong to topotype III (WZ) (see below).

[OIE Immediate notification & Follow-up reports](#)

#### The Republic of Malawi

An outbreak of FMD type SAT 2 was previously reported in cattle at Kasokeza, Maperera Dip tank, Chikwawa, Southern Region on 7 August 2020. VP1 sequencing was performed at the OIE Sub-Saharan Africa Regional Reference laboratory (SSARRL) for FMD at the Botswana Vaccine Institute (BVI) on two samples and showed that the virus belonged to topotype I (see below).

[OIE Immediate notification & Follow-up reports](#)

#### The Republic of Namibia

Between 25 September 2020 and 25 October 2020, four outbreaks of FMD type SAT 2 were reported in cattle in the Kavango East and Kavango West regions. No genotyping has been reported.

[OIE Immediate notification & Follow-up reports](#)
The Republic of South Africa

Between 03 September 2020 and 23 October 2020, three outbreaks of FMD type SAT 1 were reported in cattle in Greater Giyani, Limpopo. Diagnosis of these sub-clinical cases was performed using serological methods and no genotyping has been reported.

OIE Immediate notification & Follow-up reports

The Republic of Uganda

A batch of 11 samples was received to WRLFMD on 16 December 2020. Typing and genotyping is underway and results will be reported shortly.

The Republic of Zimbabwe

An outbreak of FMD (untyped) was reported in cattle on 12/10/2020 at Chinyika, Bikita, Masvingo.

OIE Immediate notification & Follow-up reports

3.8. Pool 7 (South America)

No new outbreaks of FMD were reported in South America.

3.9. Extent of global surveillance

Figure 3: Samples received during 2019 from FMD outbreaks (routine surveillance that is undertaken in countries that are FMD-free without vaccination is not shown). Data from presentations given at the OIE/FAO Reference
In regions where FMD is endemic, continuous evolution of the virus generates geographically discrete lineages that are genetically distinct from FMD viruses found elsewhere. This report displays how different FMD lineages circulate in different regions; these analyses accommodate the latest epidemiological intelligence to assess the relative importance of the viral strains circulating within each regions (see Table 1, below).
**Table 1**: Conjectured relative prevalence of circulating FMD viral lineages in each Pool. For each of the regions, data represent the relative importance of each viral lineage [prevalence score estimated as a percentage (%) of total FMD cases that occur in domesticated hosts]. These scores (reviewed at the OIE/FAO FMD Laboratory Network meeting in December 2020) can be used to inform the PRAGMATIST tool (see Annex 3). Recent changes to increase risks are shown in red, while a reduction in risk is shown in green.

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<td></td>
<td></td>
</tr>
<tr>
<td>O EURO-SA</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>80</td>
</tr>
<tr>
<td>O CATHAY</td>
<td>10.5</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A ASIA Sea-97</td>
<td>26</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A ASIA Iran-05</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A ASIA G-VII</td>
<td>16</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>27</td>
</tr>
<tr>
<td>A AFRICA</td>
<td>25</td>
<td>22</td>
<td>15</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A EURO-SA</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>20</td>
</tr>
<tr>
<td>Asia-1</td>
<td>0.5</td>
<td>4</td>
<td>12.5</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SAT 1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SAT 2</td>
<td>0.5</td>
<td>10</td>
<td>14</td>
<td>10</td>
<td>57</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SAT 3</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>16</td>
</tr>
<tr>
<td>C</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

A number of outbreaks have occurred where samples have not been sent to the WRLFMD or other laboratories in the OIE/FAO FMD Laboratory Network. An up-to-date list and reports of FMD viruses characterised by sequencing can be found at the following website: [http://www.wrlfmd.org/country-reports/country-reports-2020](http://www.wrlfmd.org/country-reports/country-reports-2020).

Results from samples or sequences received at WRLFMD (status of samples being tested) are shown in Table 2 and a complete list of clinical sample diagnostics made by the WRLFMD from October to December 2020 is shown in Annex 1: (Summary of submissions). A record of all samples received by WRLFMD is shown in Annex 1: (Clinical samples).
Table 2: Status of sequencing of samples or sequences received by the WRLFMD from October to December 2020 (* indicates a batch carried over from the previous quarter).

<table>
<thead>
<tr>
<th>WRLFMD Batch No.</th>
<th>Date received</th>
<th>Country</th>
<th>Serotype</th>
<th>No. of samples</th>
<th>No. of sequences</th>
<th>Sequencing status</th>
</tr>
</thead>
<tbody>
<tr>
<td>WRLFMD/2020/00006</td>
<td>16/12/2020</td>
<td>Uganda</td>
<td>pending</td>
<td>11</td>
<td>-</td>
<td>pending</td>
</tr>
<tr>
<td>WRLFMD/2020/00007</td>
<td>22/12/2020</td>
<td>Thailand</td>
<td>pending</td>
<td>16</td>
<td>-</td>
<td>pending</td>
</tr>
<tr>
<td>WRLFMD/2020/00008</td>
<td>22/12/2020</td>
<td>Cambodia</td>
<td>pending</td>
<td>9</td>
<td>-</td>
<td>pending</td>
</tr>
<tr>
<td>WRLFMD/2020/00009</td>
<td>22/12/2020</td>
<td>Lao P.D.R.</td>
<td>pending</td>
<td>5</td>
<td>-</td>
<td>pending</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Total</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>41</td>
<td>-</td>
<td></td>
</tr>
</tbody>
</table>

Table 3: VP1 sequences submitted by other FMD Network laboratories to the WRLFMD from October to December 2020 (* indicates sequences retrieved from GenBank).

<table>
<thead>
<tr>
<th>WRLFMD Batch No.</th>
<th>Date received</th>
<th>Country</th>
<th>Serotype</th>
<th>Date Collected</th>
<th>No. of sequences</th>
<th>Submitting laboratory</th>
</tr>
</thead>
<tbody>
<tr>
<td>WRLMEG/2020/00026</td>
<td>06/10/2020</td>
<td>Turkey</td>
<td>O</td>
<td>2019, 2020</td>
<td>6</td>
<td>FMDI</td>
</tr>
<tr>
<td>WRLMEG/2020/00027</td>
<td>19/10/2020</td>
<td>Botswana</td>
<td>SAT 1</td>
<td>2020</td>
<td>2</td>
<td>SSARL</td>
</tr>
<tr>
<td>WRLMEG/2020/00028</td>
<td>19/10/2020</td>
<td>Malawi</td>
<td>SAT 2</td>
<td>2020</td>
<td>2</td>
<td>SSARL</td>
</tr>
<tr>
<td>WRLMEG/2020/00035</td>
<td>23/10/2020</td>
<td>Iraq</td>
<td>O</td>
<td>2019</td>
<td>2*</td>
<td>Univ. of Mosul</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Asia 1</td>
<td>2019</td>
<td>1*</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>SAT 1</td>
<td>2019</td>
<td>2*1</td>
<td></td>
</tr>
<tr>
<td>WRLMEG/2020/00036</td>
<td>25/11/2020</td>
<td>Iran</td>
<td>A</td>
<td>2020</td>
<td>6</td>
<td>CVL</td>
</tr>
<tr>
<td>WRLMEG/2020/00037</td>
<td>25/11/2020</td>
<td>Nigeria</td>
<td>O</td>
<td>2020</td>
<td>1</td>
<td>NCFAD (Canada)/ NVRI (Nigeria)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>SAT 2</td>
<td>2019</td>
<td>2</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>SAT 1</td>
<td>2015</td>
<td>6*</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>SAT 2</td>
<td>2013, 2017</td>
<td>3*</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>2*</td>
<td></td>
</tr>
<tr>
<td>WRLMEG/2020/00039A</td>
<td>28/12/2020</td>
<td>India</td>
<td>O</td>
<td>2018</td>
<td>13*</td>
<td>ICAR-DFMD</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Total</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>72</td>
</tr>
</tbody>
</table>

1 confirmation of these results requires input from OIE of FAO FMD Reference Laboratories
4. Detailed analysis

4.1. Pool 1 (Southeast Asia/Central Asia/East Asia)

Republic of India
Batch: WRLMEG/2020/00039
Sequence provided by ICAR-Directorate of FMD (GenBank)
Date received: 28/12/2020
No. of samples: 286
O (ME-SA/PanAsia): 2
O (ME-SA/Ind-2001d): 60
O (ME-SA/Ind-2001e): 211
O (ME-SA/SAR-2018): 13 (only these data are shown)
4.2. Pool 3 (West Eurasia and Middle East)

Islamic Republic of Iran
Batch: WRLMEG/2020/00036
Sequence provided by CVL-IVO
Date received: 25/11/2020
No. of samples: 6
A (ASIA/Iran-05FAR-11): 6
Republic of Turkey

Batch: WRLMEG/2020/00026

Sequence provided by FMDI-Ankara

Date received: 06/10/2020

No. of samples: 6

O (ME-SA/PanAsia-2QOM-15): 4
O (ME-SA/PanAsia-2ANT-10): 2
4.3. Pool 5 (West/Central Africa)

Federal Republic of Nigeria
Batch: WRLMEG/2020/00037
Sequence provided by NCFAD/NVRI
Date received: 25/11/2020
No. of samples: 18
O (WA): 2
A (AFRICA/G-IV): 14
SAT2 (VII): 2

Nigeria continued on next page
Nigeria Continued

Nigeria continued next page
Nigeria continued
Federal Republic of Nigeria
Batch: WRLMEG/2020/00038
Sequence provided by Sciensano (GenBank)
Date received: 11/12/2020
No. of samples: 25
O (EA-3): 12
O (WA): 2
A (AFRICA/G-IV): 6
SAT1 (X): 3
SAT2 (VII/Lib-12): 2

Nigeria continued on next page
Nigeria continued
Nigeria continued
4.4. Pool 6 (Southern Africa)

Republic of Botswana
Batch: WRLMEG/2020/00027
Sequence provided by SSARRL (BVI)
Date received: 15/10/2020
No. of samples: 2

SAT1 (III): 2
Republic of Malawi
Batch: WRLMEG/2020/00028
Sequence provided by SSARRL (BVI)
Date received: 15/10/2020
No. of samples: 2
SAT2 (I): 2
4.5. Vaccine matching

Antigenic characterisation of FMD field isolates by matching with vaccine strains by 2dmVNT from October to December 2020.

NOTES:

1. Vaccine efficacy is influenced by vaccine potency, antigenic match and vaccination regime. Therefore, it is possible that a less than perfect antigenic match of a particular antigen may be compensated by using a high potency vaccine and by administering more than one vaccine dose at suitable intervals. Thus, a vaccine with a weak antigenic match to a field isolate, as determined by serology, may nevertheless afford some protection if it is of sufficiently high potency and is administered under a regime to maximise host antibody responses (Brehm, 2008).

2. Vaccine matching data generated in this report only considers antibody responses in cattle after a single vaccination (typically 21 days after vaccination). The long-term performance of FMD vaccines after a second or multiple doses of vaccine should be monitored using post-vaccination serological testing.

Table 4: Summary of samples tested by vaccine matching

<table>
<thead>
<tr>
<th>Serotype</th>
<th>O</th>
<th>A</th>
<th>C</th>
<th>Asia-1</th>
<th>SAT 1</th>
<th>SAT 2</th>
<th>SAT 3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pakistan*</td>
<td>2</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Vietnam*</td>
<td>4</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
</tbody>
</table>

* Supplementary vaccine matching reports

Abbreviations used in tables

For each field isolate the r1 value is shown followed by the heterologous neutralisation titre (r1-value / titre). The r1 values shown below, represent the one-way serological match between vaccine strain and field isolate, calculated from the comparative reactivity of antisera raised against the vaccine in question. Heterologous neutralisation titres for vaccine sera with the field isolates are included as an indicator of cross-protection.
Vaccine Match

\( r_1 \geq 0.3 \) - suggests that there is a close antigenic relationship between field isolate and vaccine strain. A potent vaccine containing the vaccine strain is likely to confer protection.

No Vaccine Match

\( r_1 < 0.3 \) - suggest that the field isolate is antigenically different to the vaccine strain. Where there is no alternative, the use of this vaccine should carefully consider vaccine potency, the possibility to use additional booster doses and monitoring of vaccinated animals for heterologous responses.

Not tested against this vaccine

NOTE: A “0” in the neutralisation columns indicates that for that particular field virus no neutralisation was observed at a virus dose of a 100 TCID\(_{50}\).

NOTE: This report includes the source of the vaccine virus and bovine vaccinal serum. Vaccines from different manufactures may perform differently and caution should be taken when comparing the data.

Table 5: Supplementary vaccine matching studies for O1 Campos

<table>
<thead>
<tr>
<th>Isolate</th>
<th>Serotype O</th>
<th>O1 Campos Biogenesis</th>
<th>( r_1 )-value</th>
<th>Titre</th>
</tr>
</thead>
<tbody>
<tr>
<td>PAK/46/2019</td>
<td>ME-SA Ind-2001</td>
<td></td>
<td>0.26</td>
<td>1.90</td>
</tr>
<tr>
<td>VIT/13/2020</td>
<td>ME-SA Ind-2001</td>
<td></td>
<td>0.78</td>
<td>2.24</td>
</tr>
<tr>
<td>VIT/19/2019</td>
<td>ME-SA PanAsia</td>
<td></td>
<td>0.79</td>
<td>2.24</td>
</tr>
<tr>
<td>PAK/3/2020</td>
<td>ME-SA PanAsia-2</td>
<td></td>
<td>0.56</td>
<td>2.19</td>
</tr>
<tr>
<td>VIT/15/2019</td>
<td>SEA Mya-98</td>
<td></td>
<td>0.15</td>
<td>1.61</td>
</tr>
<tr>
<td>VIT/31/2019</td>
<td>SEA Mya-98</td>
<td></td>
<td>0.24</td>
<td>1.82</td>
</tr>
</tbody>
</table>
**Table 6:** Supplementary vaccine matching studies for O PanAsia-2

<table>
<thead>
<tr>
<th>Isolate</th>
<th>Serotype O</th>
<th>Topotype</th>
<th>Lineage</th>
<th>r₁-value</th>
<th>Titre</th>
</tr>
</thead>
<tbody>
<tr>
<td>TUN/1/2019</td>
<td>O PanAsia-2</td>
<td>EA-3</td>
<td>-</td>
<td>0.65</td>
<td>2.12</td>
</tr>
<tr>
<td>MOR/1/2019</td>
<td>EA-3</td>
<td>-</td>
<td>-</td>
<td>0.49</td>
<td>2.00</td>
</tr>
<tr>
<td>ALG/1/2019</td>
<td>EA-3</td>
<td>-</td>
<td>-</td>
<td>0.59</td>
<td>2.08</td>
</tr>
<tr>
<td>SRL/14/2019</td>
<td>ME-SA</td>
<td>-</td>
<td>-</td>
<td>0.28</td>
<td>1.93</td>
</tr>
<tr>
<td>SRL/1/2019</td>
<td>ME-SA</td>
<td>Ind-2001d</td>
<td>-</td>
<td>0.39</td>
<td>2.08</td>
</tr>
<tr>
<td>SRL/17/2019</td>
<td>ME-SA</td>
<td>Ind-2001d</td>
<td>-</td>
<td>0.29</td>
<td>1.95</td>
</tr>
<tr>
<td>BHU/1/2019</td>
<td>ME-SA</td>
<td>Ind-2001e</td>
<td>-</td>
<td>0.58</td>
<td>2.07</td>
</tr>
<tr>
<td>PAK/46/2019</td>
<td>ME-SA</td>
<td>Ind-2001e</td>
<td>-</td>
<td>0.62</td>
<td>2.28</td>
</tr>
<tr>
<td>PAK/12/2019</td>
<td>ME-SA</td>
<td>PanASIA-2</td>
<td>ANT-10</td>
<td>0.32</td>
<td>2.00</td>
</tr>
<tr>
<td>PAT/3/2019</td>
<td>ME-SA</td>
<td>PanASIA-2</td>
<td>QOM-15</td>
<td>0.39</td>
<td>1.90</td>
</tr>
<tr>
<td>TUR/4/2019</td>
<td>ME-SA</td>
<td>PanASIA-2</td>
<td>QOM-15</td>
<td>0.51</td>
<td>2.02</td>
</tr>
<tr>
<td>PAK/3/2020</td>
<td>ME-SA</td>
<td>PanASIA-2</td>
<td>ANT-10</td>
<td>0.36</td>
<td>2.05</td>
</tr>
</tbody>
</table>
Annex 1: Sample data

Summary of submissions

Table 7: Summary of samples collected and received to WRLFMD (October to December 2020)

<table>
<thead>
<tr>
<th>Country</th>
<th>No. of samples</th>
<th>Virus isolation in cell culture/ELISA</th>
<th>FMD virus serotypes</th>
<th>No Virus Detected</th>
<th>RT-PCR for FMD</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>O</td>
<td>A</td>
<td>C</td>
</tr>
<tr>
<td>Cambodia</td>
<td>9</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lao P.D.R.</td>
<td>5</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Thailand</td>
<td>16</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Uganda</td>
<td>11</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>TOTAL</strong></td>
<td><strong>41</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Clinical samples

Table 8: Clinical sample diagnostics made by the WRLFMD® October to December 2020

<table>
<thead>
<tr>
<th>Country</th>
<th>Received</th>
<th>Reported</th>
<th>WRL for FMD Sample Identification</th>
<th>Animal</th>
<th>Date of Collection</th>
<th>VI/ELISA</th>
<th>RT-PCR</th>
<th>Final report</th>
</tr>
</thead>
</table>

**TOTAL** 0
Annex 2: FMD publications

Recent FMD Publications (October to December 2020) cited by Web of Science.


Foot-and-mouth disease virus 3B protein interacts with pattern recognition receptor RIG-I to block RIG-I-mediated immune signaling and inhibit host antiviral response. 
Journal of Immunology, 205(8): 2207-2221. DOI: 10.4049/jimmunol.1901333.

Optimized adenoviral vector that enhances the assembly of FMDV O virus-like particles in situ increases its potential as vaccine for serotype O viruses. 
Annex 3: Vaccine recommendations

This report provides recommendations of FMDV vaccines to be included in antigen banks. These outputs are generated with a new tool (called PRAGMATIST) that has been developed in partnership between WRLFMD and EuFMD. These analyses accommodate the latest epidemiological data collected by the OIE FAO FMD Laboratory Network regarding FMDV lineages that are present in different source regions (see Table 1 in Section 3.9, above), as well as available in vitro, in vivo and field data to score the ability of vaccines to protect against these FMDV lineages.

Vaccine Antigen Prioritisation: Europe
October 2020

Please contact WRLFMD or EuFMD for assistance to tailor these outputs to other geographical regions. NB: Vaccine-coverage data presented is based on available data and may under-represent the true performance of individual vaccines.
Annex 4: Brief round-up of EuFMD and WRLFMD activities

Courses

EuFMD’s open access online courses provide convenient self-paced training which you may study anytime, anywhere, free of charge. Link to all courses: https://eufmdlearning.works/mod/page/view.php?id=13130

- There are currently 4 courses in English, 1 in French and 1 in Arabic:
  - Introduction to Foot-and-Mouth Disease (in English, French and Arabic)
  - What is the Progressive Control Pathway?
  - Public Private Partnerships in the Veterinary Domain (in support of OIE Training)
  - Introduction to the Progressive Control Pathway
  - Introduction to the Risk-based Strategic Plan (RBSP) *coming soon*

- The WRLFMD residential training course on FMD diagnostics (https://www.pirbright.ac.uk/instructor-led-training/diagnosis-foot-and-mouth-disease) scheduled for May 2020 has been postponed.

Podcasts

We have a constantly updated series of short podcasts relating to the FAST world, available here: http://www.fao.org/eufmd/resources/podcasts/en/

Meetings

- The EuFMD Open Session will conclude on 16 February (https://www.eufmd.info/os20faster)
- 44th General Session of the EuFMD will be held 21 April 2021 - 23 April 2021
- GFRA conferences for America (15 March) and South East Asia (week of 22 March).
**Proficiency test scheme organised by WRLFMD**

Sample panels for the Phase XXXII exercise have shipped to international laboratories; however, this is still ongoing as the disruption to air travel continues. Results have been received from laboratories and these are currently being analysed (see table below for a summary of the current status of the exercise).

<table>
<thead>
<tr>
<th>Status</th>
<th>Number of Labs</th>
</tr>
</thead>
<tbody>
<tr>
<td>Invitations</td>
<td>72</td>
</tr>
<tr>
<td>Declined to take part</td>
<td>9</td>
</tr>
<tr>
<td>Paperwork in progress</td>
<td>1</td>
</tr>
<tr>
<td>Awaiting shipping</td>
<td>2</td>
</tr>
<tr>
<td>Panels shipped</td>
<td>35</td>
</tr>
<tr>
<td>Destroyed in transit</td>
<td>1</td>
</tr>
<tr>
<td>Results returned</td>
<td>26</td>
</tr>
</tbody>
</table>

We will write to inform participating laboratories about any other changes that may be required to accommodate these events, and please feel free to contact WRLFMD if you have any questions.
Hold-FAST tools

EuFMD Committees
Executive Committee, Standing Technical Committee, Special Committee for Surveillance and Applied Research (SCSAR), Special Committee on Biorisk Management (SCBRM), Tripartite Groups.